

<!--StartFragment-->RESULT 1

KIRR2_MOUSE

ID KIRR2_MOUSE Reviewed; 700 AA.

AC Q7TSU7; Q7TQ98;

DT 25-OCT-2004, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-2003, sequence version 1.

DT 24-JUL-2007, entry version 34.

DE Kin of IRRE-like protein 2 precursor (Kin of irregular chiasm-like protein 2).

GN Name=Kirrel2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORM 1).

RC TISSUE=Olfactory epithelium;

RX PubMed=15489334; DOI=10.1101/gr.2596504;

RG The MGC Project Team;

RT "The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC).";

RL Genome Res. 14:2121-2127(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE [mRNA] OF 48-376 (ISOFORM 2), AND TISSUE SPECIFICITY.

RX MEDLINE=22721688; PubMed=12837264; DOI=10.1016/S0888-7543(03)00110-1;

RA Sun C., Kilburn D., Lukashin A., Crowell T., Gardner H., Brundiers R., Diefenbach B., Carulli J.P.;

RT "Kirrel2, a novel immunoglobulin superfamily gene expressed primarily in beta cells of the pancreatic islets.";

RL Genomics 82:130-142(2003).

RN [3]

RP INTERACTION WITH NPHS2, AND TISSUE SPECIFICITY.

RC STRAIN=Swiss Webster; TISSUE=Brain;

RX PubMed=12424224; DOI=10.1096/fj.02-0242fje;

RA Sellin L., Huber T.B., Gerke P., Quack I., Pavenstaedt H., Walz G.;

RT "NEPH1 defines a novel family of podocin interacting proteins.";

RL FASEB J. 17:115-117(2003).

CC -!- SUBUNIT: Interacts with C-terminus of NPHS2/podocin.

CC -!- SUBCELLULAR LOCATION: Membrane; Single-pass type I membrane protein (Potential).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q7TSU7-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q7TSU7-2; Sequence=VSP_011786;

CC -!- TISSUE SPECIFICITY: Highly expressed in beta-cells of the pancreatic islets. Expressed also in podocytes of kidney glomeruli.

CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.

CC -!- SIMILARITY: Contains 5 Ig-like C2-type (immunoglobulin-like) domains.

CC -----

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CC -----

DR EMBL; BC052773; AAH52773.1; -; mRNA.

DR EMBL; AY305303; AAP72168.1; -; mRNA.

DR UniGene; Mm.113908; -.

DR Ensembl; ENSMUSG00000036915; Mus musculus.
 DR MGI; MGI:2442334; Kirrel2.
 DR InterPro; IPR013162; CD80_C2-set.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR013783; Ig-like_fold.
 DR InterPro; IPR013098; Ig_I-set.
 DR InterPro; IPR003599; Ig_sub.
 DR InterPro; IPR003598; Ig_sub2.
 DR InterPro; IPR013106; Ig_V-set.
 DR Gene3D; G3DSA:2.60.40.10; Ig-like_fold; 3.
 DR Pfam; PF08205; C2-set_2; 1.
 DR Pfam; PF07679; I-set; 2.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGc2; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 PE 1: Evidence at protein level;
 KW Alternative splicing; Glycoprotein; Immunoglobulin domain; Membrane;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 700 Kin of IRRE-like protein 2.
 /FTId=PRO_0000015097.
 FT TOPO_DOM 20 507 Extracellular (Potential).
 FT TRANSMEM 508 528 Potential.
 FT TOPO_DOM 529 700 Cytoplasmic (Potential).
 FT DOMAIN 21 115 Ig-like C2-type 1.
 FT DOMAIN 120 219 Ig-like C2-type 2.
 FT DOMAIN 224 304 Ig-like C2-type 3.
 FT DOMAIN 309 391 Ig-like C2-type 4.
 FT DOMAIN 395 497 Ig-like C2-type 5.
 FT MOTIF 146 148 Cell attachment site (Potential).
 FT CARBOHYD 140 140 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 298 298 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 481 481 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 42 100 By similarity.
 FT DISULFID 143 201 By similarity.
 FT DISULFID 245 288 By similarity.
 FT DISULFID 330 372 By similarity.
 FT DISULFID 416 482 By similarity.
 FT VAR_SEQ 118 136 Missing (in isoform 2).
 /FTId=VSP_011786.
 FT CONFLICT 48 48 R -> W (in Ref. 2).
 FT CONFLICT 166 166 G -> A (in Ref. 2).
 FT CONFLICT 376 376 P -> A (in Ref. 2).
 SQ SEQUENCE 700 AA; 74529 MW; 5D9404C2E13B18B8 CRC64;

 Query Match 99.7%; Score 3678; DB 1; Length 700;
 Best Local Similarity 99.6%; Pred. No. 1.3e-224;
 Matches 697; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 MLASALLVFLCCFKGHAGSSPHFLQQPEDMVLLGEEARLPCALGAYRGLVQWTKDGLAL 60
 |||||||
 Db 1 MLASALLVFLCCFKGHAGSSPHFLQQPEDMVLLGEEARLPCALGAYRGLVQWTKDGLAL 60

 Qy 61 GGERDLPGPSRYWISGNSASGQHDLHIKPVELEDEASYECQASQAGLRSRPAQLHVMVPP 120
 |||||||
 Db 61 GGERDLPGPSRYWISGNSASGQHDLHIKPVELEDEASYECQASQAGLRSRPAQLHVMVPP 120

 Qy 121 EAPQVLGGPSVSLVAGVPGNLTCSRSGDSRPAPELLWFRDGIRLDASSFHQTTLKDKATG 180
 |||||||
 Db 121 EAPQVLGGPSVSLVAGVPGNLTCSRSGDSRPAPELLWFRDGIRLDGSSFHQTTLKDKATG 180

Qy 181 TVENTLFLTPSSHDDGATLICRARSQALPTGRDTAVTLSLQYPPMVTLSAEPQTVQEGER 240
|||
Db 181 TVENTLFLTPSSHDDGATLICRARSQALPTGRDTAVTLSLQYPPMVTLSAEPQTVQEGER 240

Qy 241 VTFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVADATFLTEPVSCESNAVGSANRS 300
|||
Db 241 VTFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVADATFLTEPVSCESNAVGSANRS 300

Qy 301 TALEVLYGPILQAKPKSVSDVGKDASFSCWRGNPLPRITWTRMGGSQLSSGPTLRP 360
|||
Db 301 TALEVLYGPILQAKPKSVSDVGKDASFSCWRGNPLPRITWTRMGGSQLSSGPTLRP 360

Qy 361 SVALEDAGDYVCRAEPRRTGLGGGKAQARLTNVNAPPVTALQPAPAFLRGPRLQCVVFA 420
|||
Db 361 SVALEDAGDYVCRAEPRRTGLGGGKAQARLTNVNAPPVTALQPAPAFLRGPRLQCVVFA 420

Qy 421 SPAPDSVVWSWDEGFLEAGSLGRFLVEAFPAPEVEGGQGPGLISVLHISGTQESDFTTGF 480
|||
Db 421 SPAPDSVVWSWDEGFLEAGSLGRFLVEAFPAPEVEGGQGPGLISVLHISGTQESDFTTGF 480

Qy 481 NCSARNRLGEGRVQIHLGRDLLPTVRIVAGAASAATSLLMVTGVVLCCWRHGSLSKQK 540
|||
Db 481 NCSARNRLGEGRVQIHLGRDLLPTVRIVAGAASAATSLLMVTGVVLCCWRHGSLSKQK 540

Qy 541 NLVRIPGSSEGSSSRGPEETGSSEDRGPIVHTDHSDLVLEEKEALETKDPTNGYYKVRG 600
|||:
Db 541 NLVRIPGSSEGSSSRGPEETGSSEDRGPIVHTDHSDLVLEEKEALETKDPTNGYYKVRG 600

Qy 601 VSVSLSLGEAPGGGLFLPPPSPIGLPGTPTYDFKPHLDLVPPCRLYRARAGYLTTPHPR 660
|||
Db 601 VSVSLSLGEAPGGGLFLPPPSPIGLPGTPTYDFKPHLDLVPPCRLYRARAGYLTTPHPR 660

Qy 661 AFTSYMKTSGPPDLSSGTPPFPYATLSPPSHQLQTHV 700
|||:
Db 661 AFTSYMKTSGPPELSSGTPPFPYATLSPPSHQLQTHV 700

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